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Figure 1

1 agatcatgcatcggttgagccgcttggtggg
 31 cgagacgggctcgatgggctccccgagcgggcacgcgggctcgatgaagtactcc
 85 ccgtgcttcacttctgcgccacgggtgatctccttgggtcgggtccaagccgaaa
 139 cctagctccggggacctcccctcgcccgccgggagctcgcccgaagccctac
 193 cccgcggatcgacgcgtcgccgcgtcgccggcgccggcgagggtacaaggcc
 247 atgtcccccgcgccggtgcccagctctcgccgagtcctgcctcaccatccccgcc
 M S P A R L P I S R E S C L T I P A 18
 301 ggcttcagccccctcagcgctcctcgactcccccggtgctcctcaccaacttcaag
 G F S P S A L L D S P V L L T N F K 36
 355 gttgaaccttcaccaacaactggtagtctgggcatggctgcgattctgcacaag
 V E P S P T T G S L G M A A I L H K 54
 409 agcgctcatccagacatgctgccttcgccacgggataaatctgttcgtaatgcc
 S A H P D M L P S P R D K S V R N A 72
 463 catgaagataggggttctagggattttgaattcaagcctcatctgaattcgtct
 H E D R G S R D F E F K P H L N S S 90
 517 tctcaatcactggctcctgctatgagtgatctaaaaaacatgagcattctatg
 S Q S L A P A M S D L K K H E H S M 108
 571 caaaatcagagtatgaatcccagctcatcatctagcaaatatggtgaataaac
 Q N Q S M N P S S S S S N M V N E N 126
 625 agacctccctgttcacgtgagtcgagcttaccagtgaatgtaagtgcacgaac
 R P P C P R E S S L T V N V S A Q N 144
 679 caacctgttggaatggttggttgactgacagcatgcctgctgaagttggtaca
 Q P V G M V G L T D S M P A E V G T 162
 733 tctgagccgcagcagatgaatagctctgacaatgccatgcaagagccgcagctct
 S E P Q Q M N S S D N A M Q E P Q S 180
 787 gaaaatgttgctgacaagtcggcagatgatggctacaactggcggaataacggg
 E N V A D K S A D D G Y N W R K Y G 198
 841 cagaagcatgtcaagggaagtgaaccctagaagttactacaagtcacacat
 Q K H V K G S E N P R S Y Y K C T H 216
 895 cctaattgtgaagtaaaaaagctattggagcgtgcagttgatggtctgatcacg
 P N C E V K K L L E R A V D G L I T 234
 949 gaagttgtctataagggaagccacaatcctcctaagccccagcccaataggagg
 E V V Y K G R H N H P K P Q P N R R 252
 1003 ttgctgggtggtgcagttccttcaaacagggtgaagaacgatatgacggcgcct
 L A G G A V E S N Q G G E E R Y D G A 270
 1057 tcagctgctgatgataaatcttccaatgctcttagcaaccttgctaattccggta
 S A A D D K S S N A L S N L A N P V 288
 1111 cattcgccctggtatggttgagcctgttcacagcttcagttagtgtgatgacatc
 H S P G M V E P V P A S V S D D I 306
 1165 gatgctggaggtggaagaccctaccctggggatgatgctactgaggaggaggat
 D A G G R P Y P G D D A T E E E D 324
 1219 tttagagtcgaaacgcaggaaatggagtcgtggtattgatgctgctgatg
 L E S K R R K M E S A G I D A A L M 342
 1273 ggtaaacctaaccgtgagccccgtgtcgttcctcaaactgtaagtgaagttgac
 G K P N R E P R V V V Q T V S E V D 360
 1327 atcttggatgatggctatcgttggcggaatatggacagaaagttgtcaaagga
 I L D D G Y R W R K Y G Q K V V K G 378
 1381 aacccaatccacggagttactacaatatgcacaagcacaggatgccctgtgagg
 N P N P R S Y Y K C T S T G C P V R 396
 1435 aagcatgttgagagagcatcacacgatcctaaatcagtgataacaacgtatgaa
 K H A V E R A S H D P K S V I T T Y E 414
 1489 ggaaaacataaccatgaagtccctgctgcgaggaatgcaaccatgagatgtcc
 G K H N H E V P A A R N A T H E M S 432
 1543 gcgcctcccataagaacgtcgtgcatcagattaacagcaatatgccagcagc
 A P P M P N V V H Q I N S N M P S S 450
 1597 attggtggcatgatgagggcatgtgaagccaggaactacaccaaccaatattct
 I G G G M M R A C E A R N Y T N Q Y S 468
 1651 caggcggctgaaaccgacactgtcagtccttgatcttgggtggttggaatcagccca
 Q A A E T D T V S L D L G V G I S P 486
 1705 aaccacagcgcagcgacaaaccaaatagcagtcctcaggtcctgaccagatgcag
 N H S D A T N Q M Q S S G P D Q M Q 504
 1759 tatcaaatgcaaacatgggttcgatgtacggcaacatgagacatccatcatca
 Y Q M Q T M G S M Y G N M R H P S S 522
 1813 atggcagcgccagcggtacaaggaactctgctgcccgcagtgatggttcgaga
 M A A V Q G N S A A R M Y G S R 540
 1867 gaagagaaaggtaacgaagggtttactttcagagocacaccgatggaccattca
 E E K G N E G F T F R A T P M D H S 558
 1921 gctaacctatgctatagcagtgctgggaacttgggtcatgggtccatgagaggga
 A N L C Y S S A G N L V M G P * 573
 1975 atgagagtgctctgcaaatgctcatagctccatgaatcatatattaccaacaatg
 2029 ctttgtaatgacaatctcttcagcaagattctcaattgtctcaattgtgtatcg
 2083 gttacaagtcagttcagccggaggcaagtagtctagtataagctatacgtgtggg
 2137 gcactgcagcaaaatacgcagtgctgtcttttaagtgcggaaaaggccctgtgtg
 2191 atgtagcatcgacgacctacattcgttgtacagcgaacctaatatgattaatta
 2245 attagattatgagaatttgggttcgtgaactgtctaattcttctgtactggaata
 2299 ttgatagaaatatagattatggtaattttctttaaaaaaaaaaaaaaaaaaaaaaa
 2353 aa

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Figure 2

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

L. b. sfl 15 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231
L. b. sfl 15 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231
L. b. hsp 15 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231
L. t. wcrk 15 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231
A. t. ent 15 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231
A. t. gsk 15 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231
A. t. d-l 15 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231
A. t. hsp 15 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231
A. t. wcrk20 15 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231
A. v. cys12a1 15 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231 GCPVNNVVERASNDH 222 VEGGHHNDVFAARH 231

[illegible][illegible]

Gene	Accession	Length (bp)	GC Content (%)
X. b. SFF1	RD000000000	549	54.9
X. b. htl	KV875LDP	739	54.9
X. b. hyp	KV875LDP	739	54.9
X. b. wcky	KV875LDP	739	54.9
A. t. gnt	KV875LDP	739	54.9
A. t. unk	KV875LDP	739	54.9
X. b. d-l	KV875LDP	739	54.9
A. t. hyp	KV875LDP	739	54.9
A. t. wcky20	KV875LDP	739	54.9

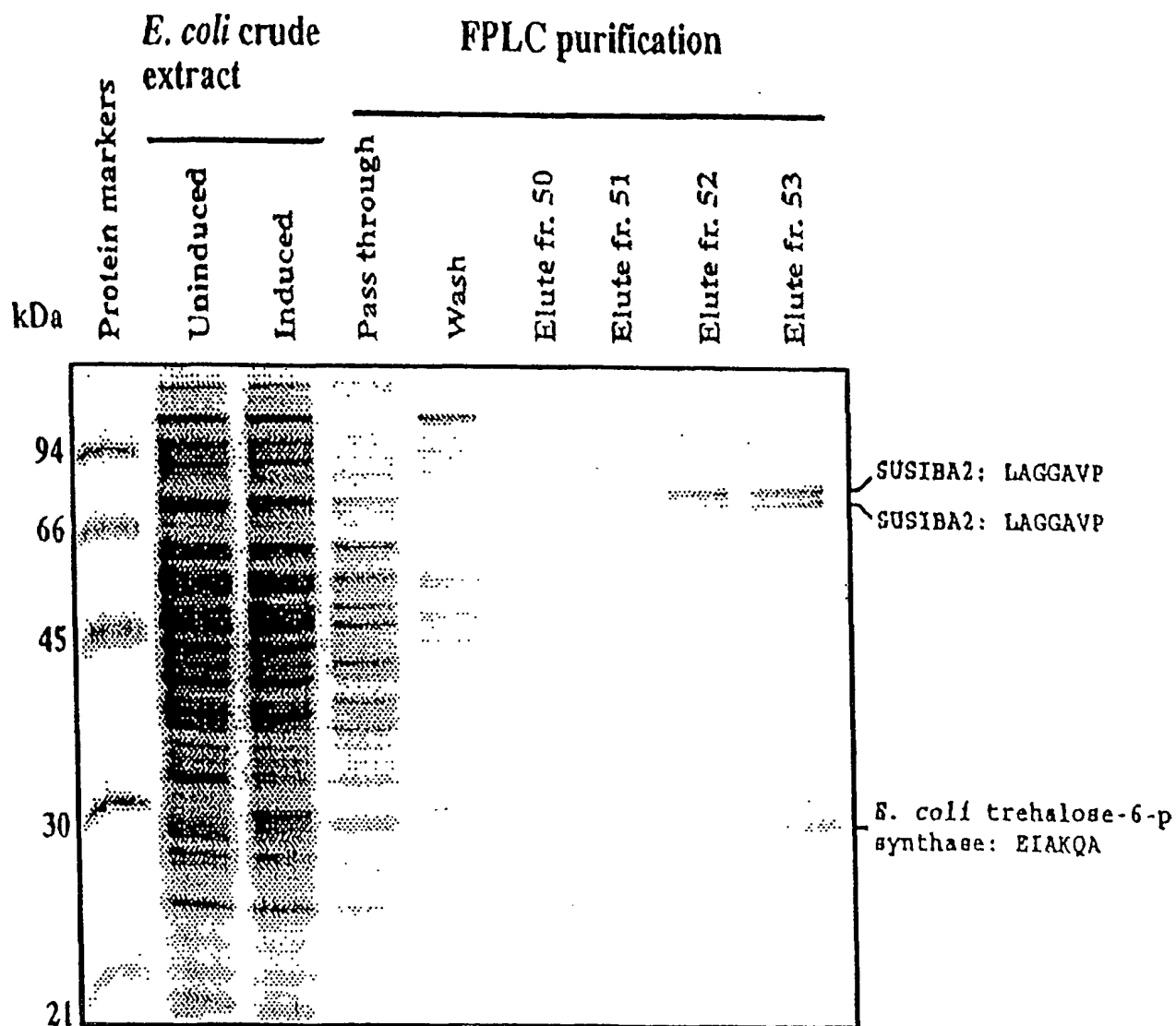
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Red

Pink

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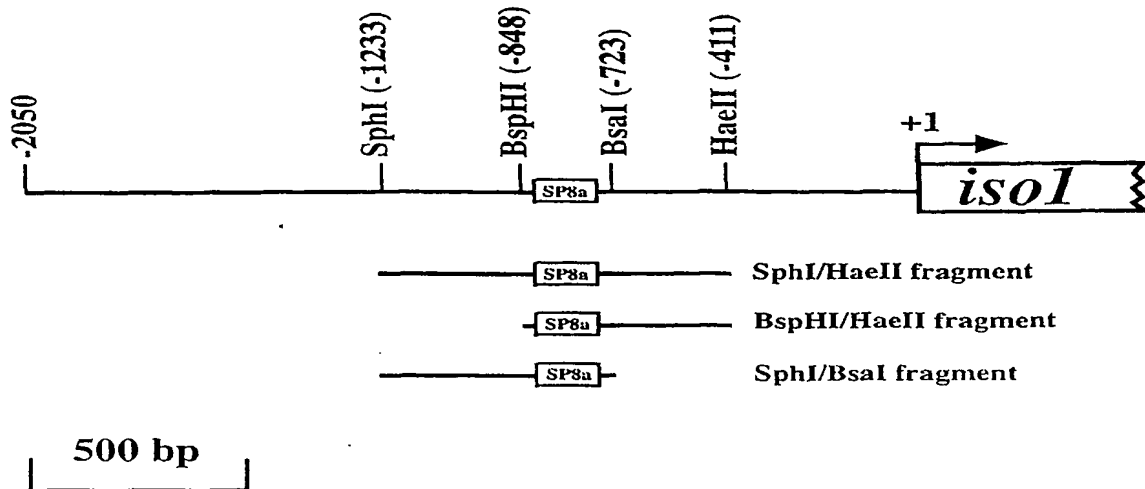
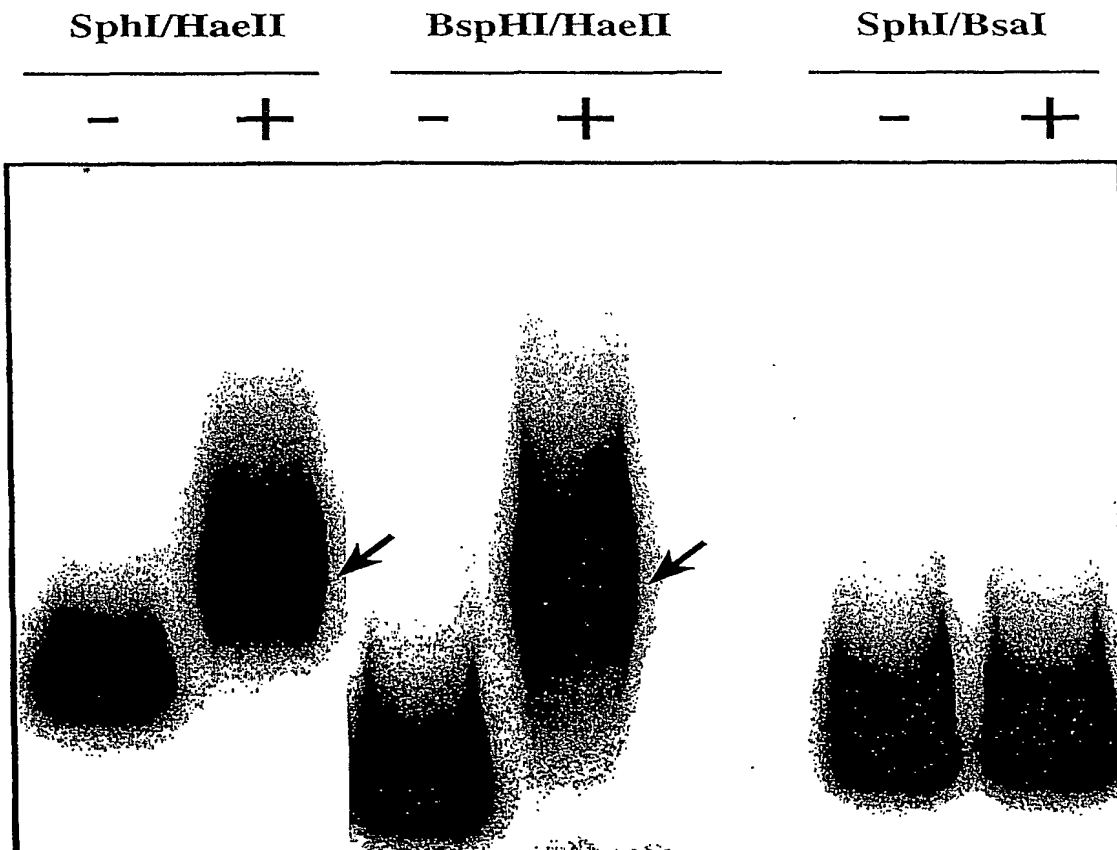
Figure 3

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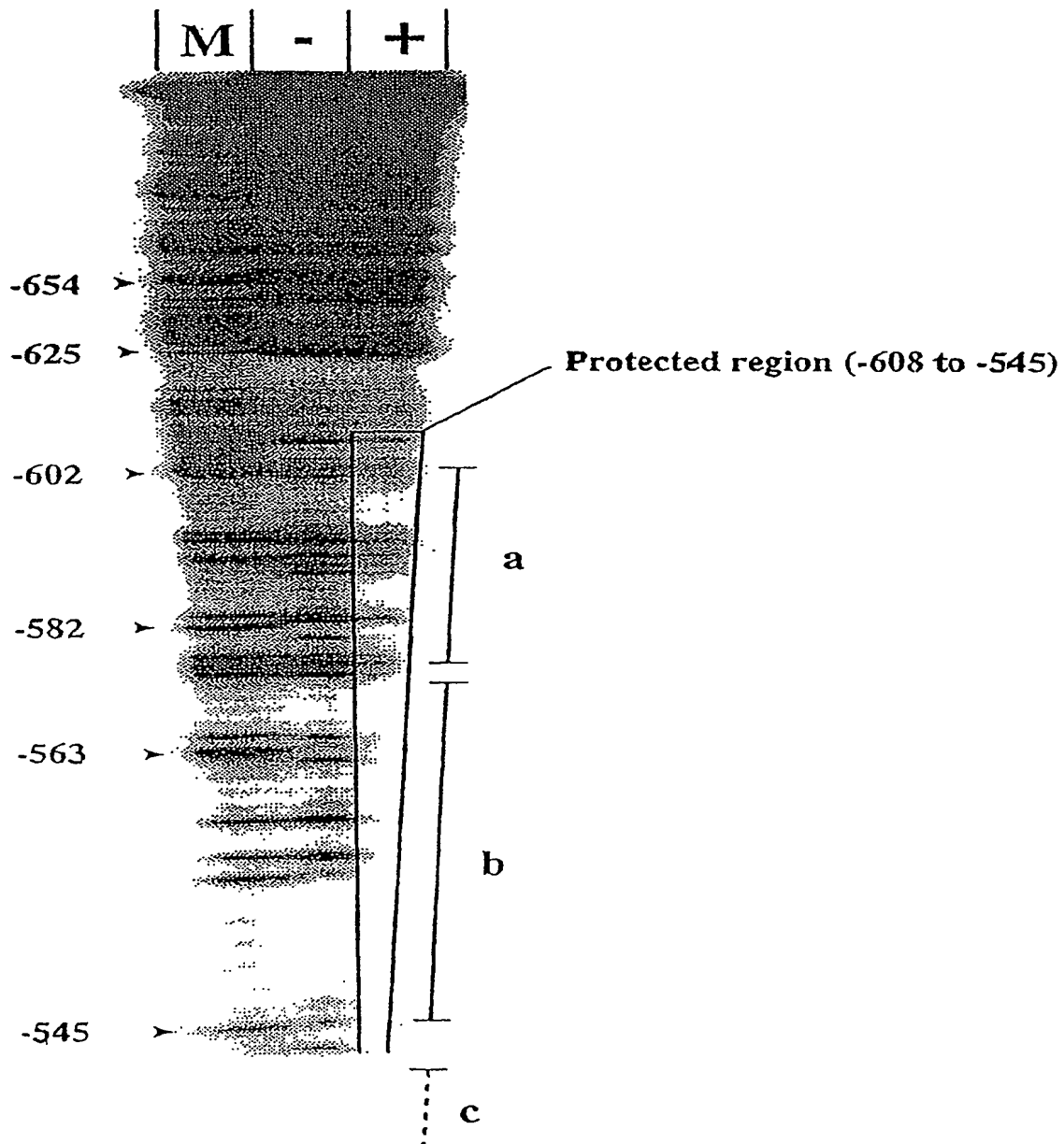
Figure 4**A**

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**B**

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Figure 5**A****B**

Protected region -603 CCGAAAAAACTAAGAAAGACCGATGGAAAA -573

Patatin SURE sequence AATACTAATAAAGA---ATAGAAAA

Protected region -568 AATACCAAAAAATAATAATAAAA -545

Patatin SURE sequence AATACTAATAAAGAATAGAAAA

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Figure 6

A

SP8a probe -772 CCCTCGTGGGAAGCAAAACTGTGTTTCTCGC -743
GGGAGCACCTTTCGTTTTGACACAAAGAGCG

SURE probe -578 GGAAAACCGAAATACCAAAAAATAATAATAAAATAATAAT -539
CCTTTTGGCTTTATGGTTTTTTATTATTATTTTATTATTA

W box probe -411 TCGCTAACCAGTGACTTCCACGTTTCATCATTTATT -376
AGCGATTGGTCACTGAAGGTGCAAAGTAGTAAATAA

B

SP8a

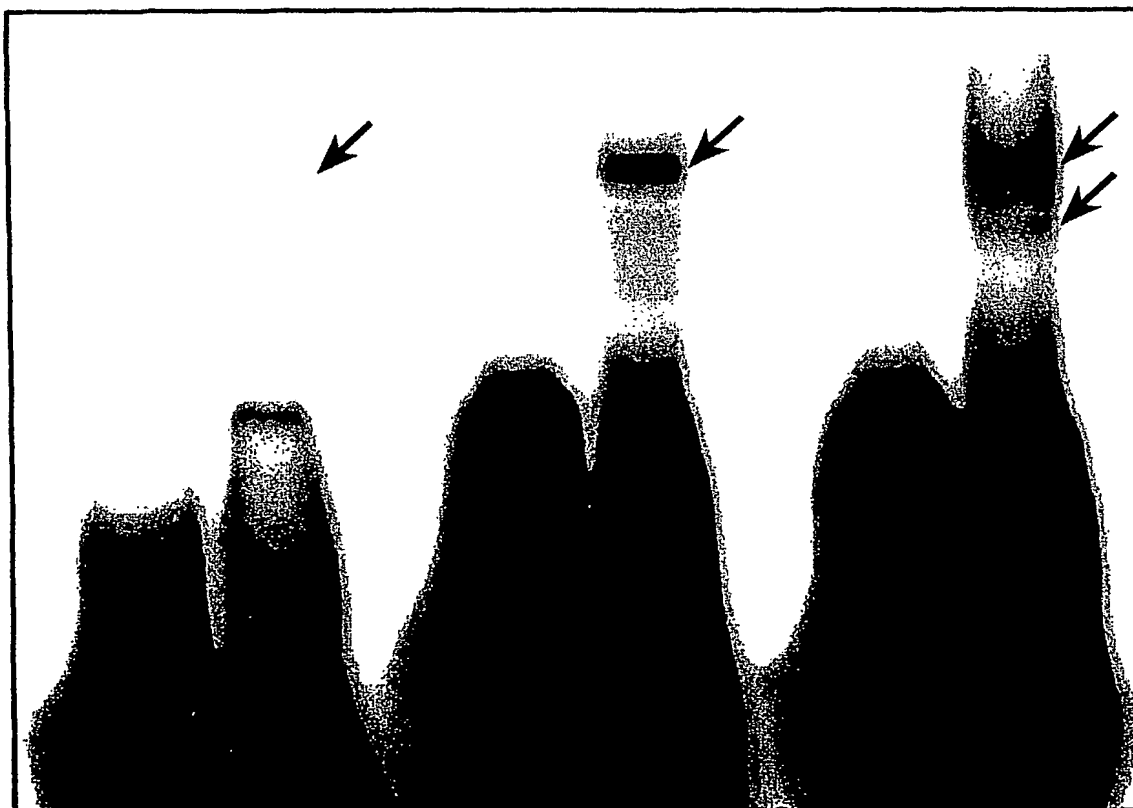
- +

SURE

- +

W box

- +

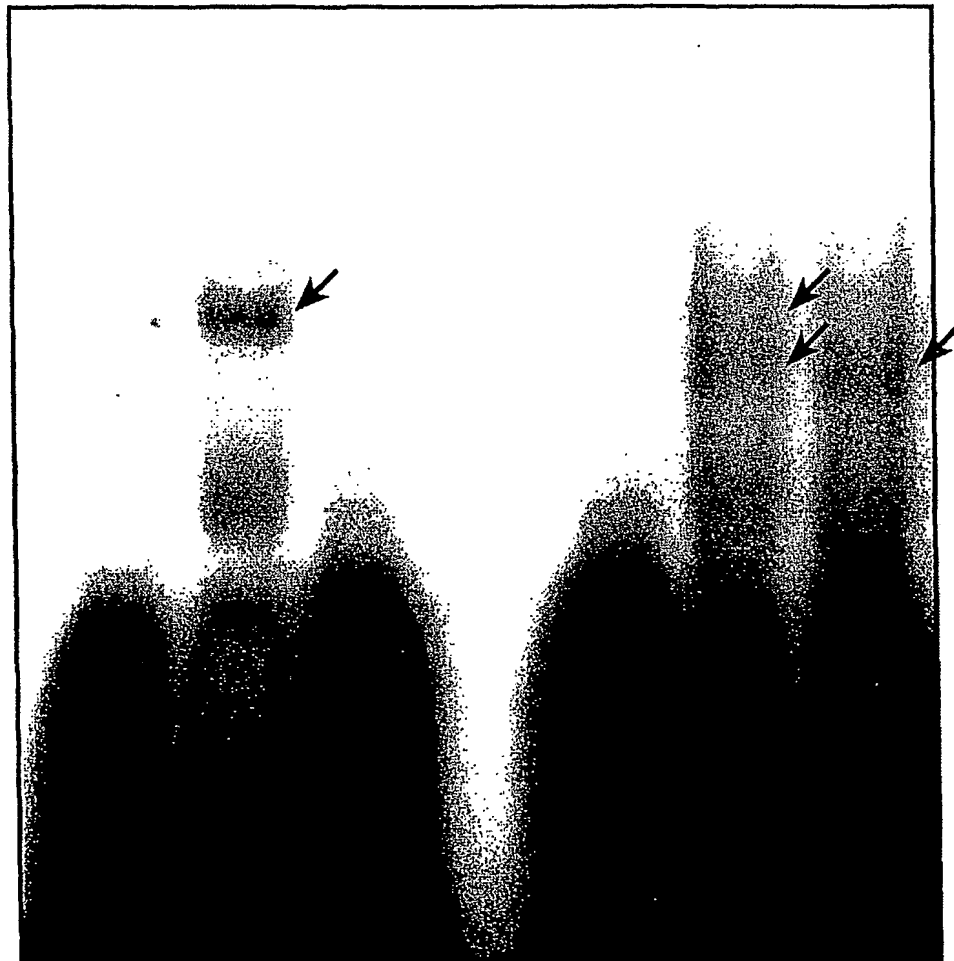


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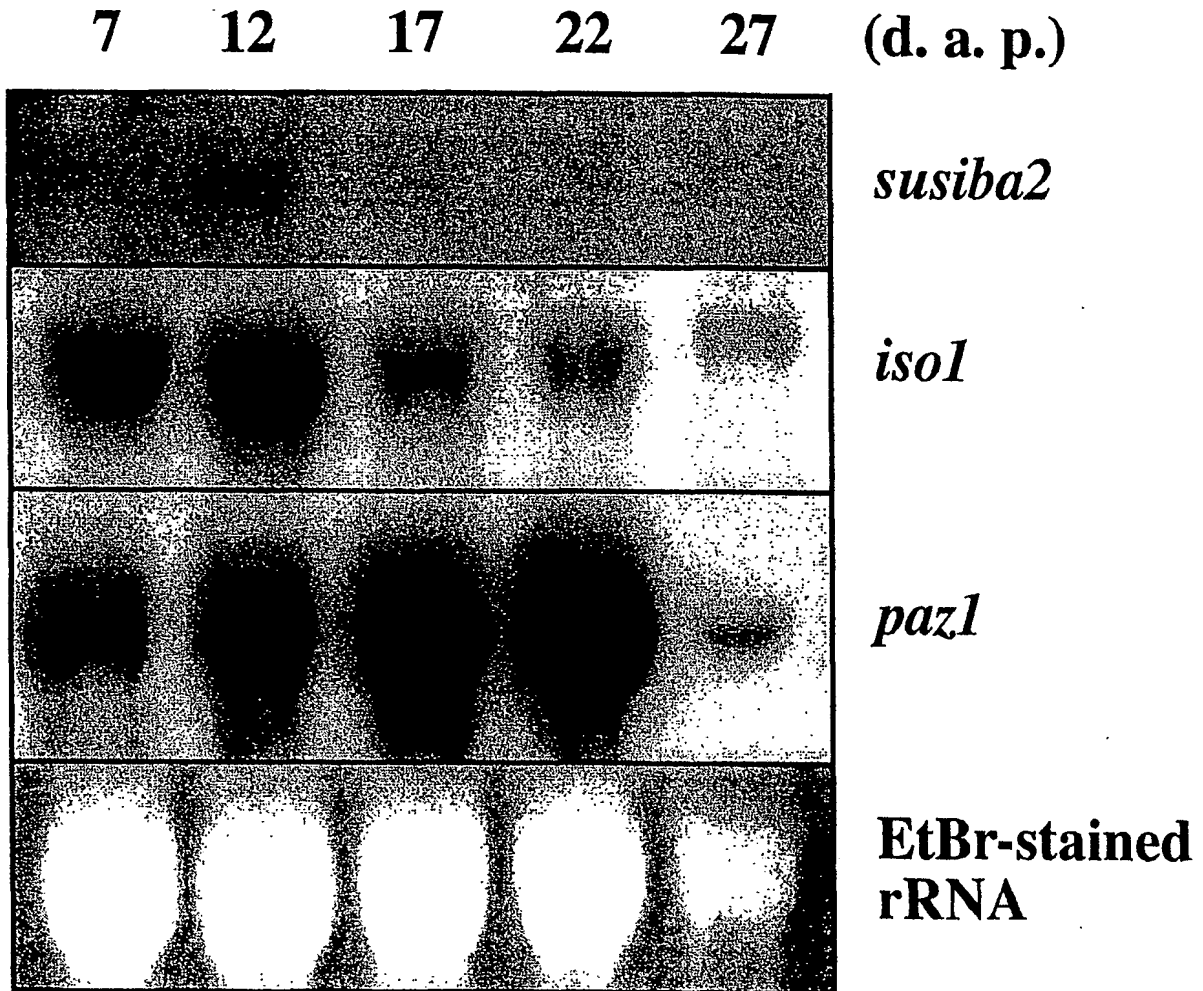
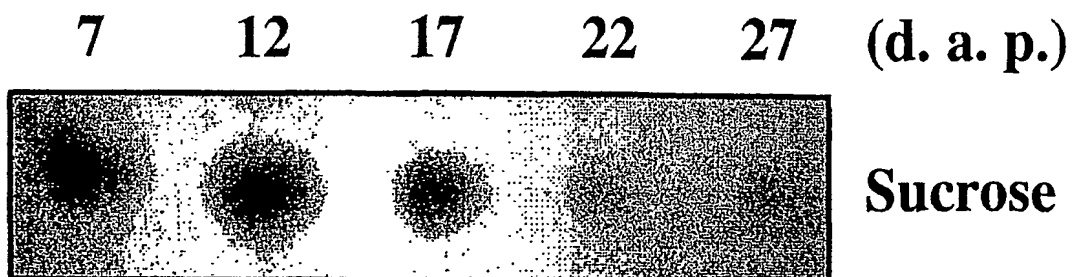
Figure 7

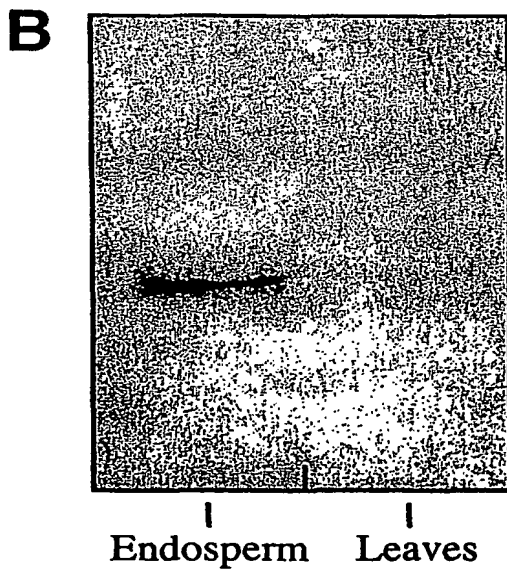
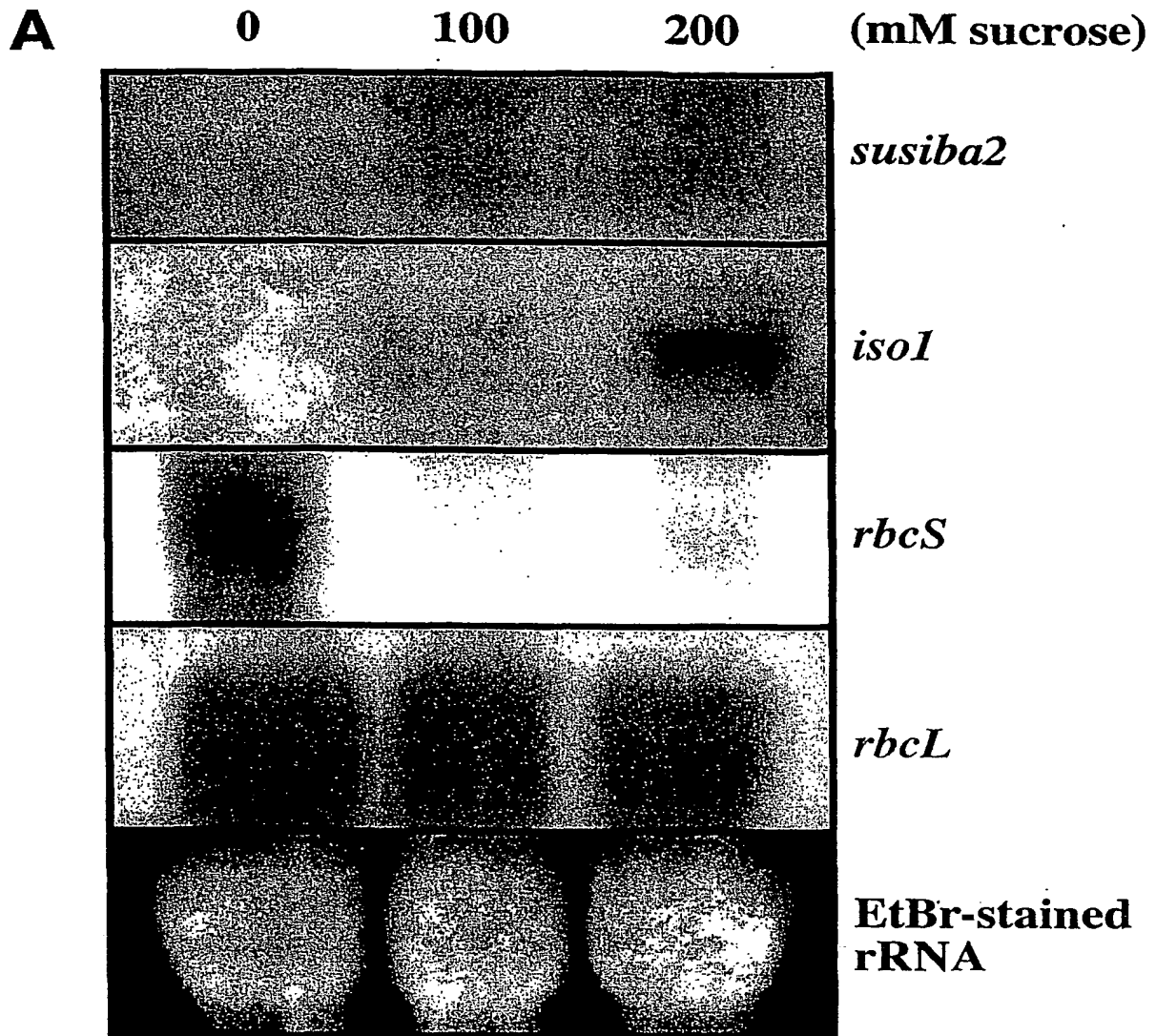
Probe:	SURE			W box		
Competitor:	-	-	W box	-	-	SURE
SUSIBA2:	-	+	+	-	+	+



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Figure 8**A****B**

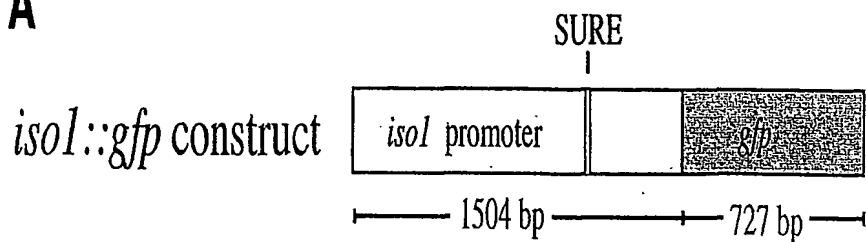
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Figure 9

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Figure 10

A

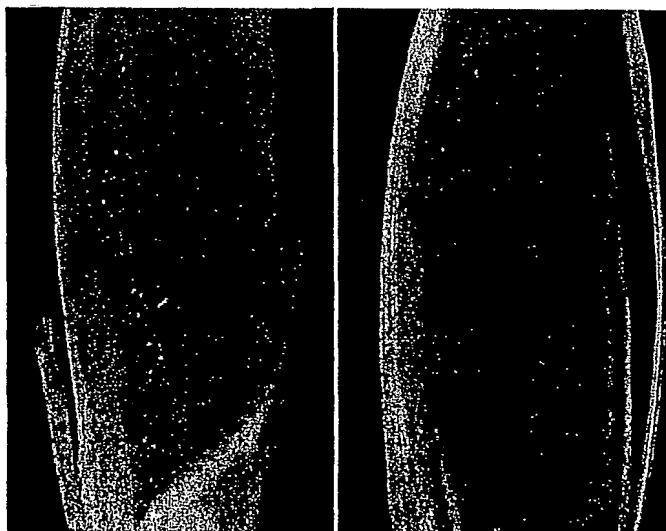


Decoy

GGAAAACCGAAATACCAAAAATAATAAAAAATAATAAT
CCTTTTGGCTTTATGGTTTTTTATTATTATTTTATTATTA

SURE

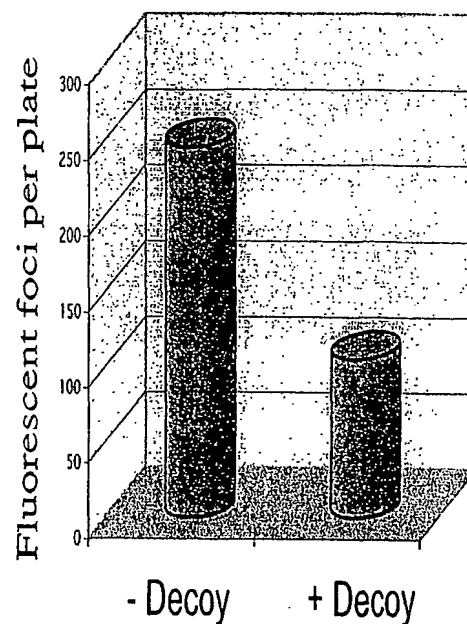
B



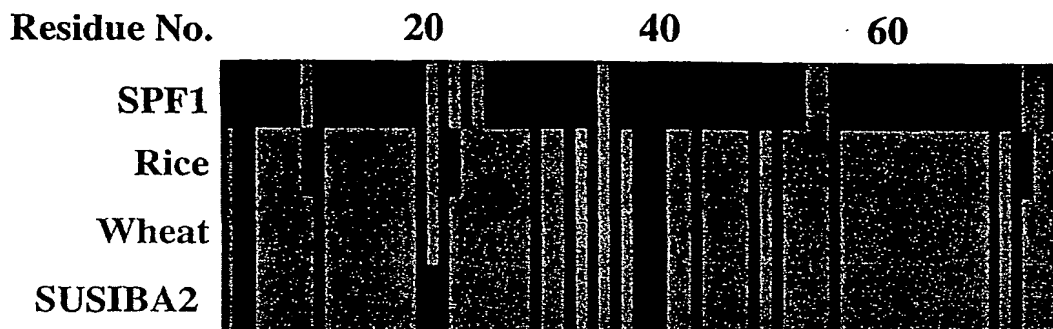
- Decoy

+ Decoy

C



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Figure 11**A**

100 % identity

Mismatch

B

SUSIBA2 MSPARLPISRESCLTIPAGFSPSALLSPVLLTNFKVEPSPTTGLGMAAILHKSAHPDM
Rice MSPARLPISREPCLTIPAGFSPSALLSPVLLTNFKVEPSPTTGLGMAAILNKSANPDI

SUSIBA2 LPSPRDKSVRNAHEDRGSRDFEFKPHLNSSSSQSLAPAMSDLKKHEHSMONOSYNPSSSSS
Rice LPSPRDKUSGSTHEDCGSRDFEFKPHLNSSSSQSLASAINDPKKHEHSMKNESLNTALSSD

SUSIBA2 NMUNENRPFCSRESSLTIVNUS-AQNOPVGMVGLTDSMPAEVGTSEPCQMNSSDNAMQEPQ
Rice DMIDNIPLCSRESSILAVNTESSAPSQLVGMVGLTDSMPAEVGTSELCQMNSSGNAMQESQ

SUSIBA2 SENVALKSADDGYNWRKYGQKHVKGSENPRSYKCTHPNCEVKKLLERAVDGLITEVVYK
Rice PESVAEKSAEDGYNWRKYGQKHVKGSENPRSYKCTHPNCDVKKLLERSIDGOITEVVYK
=====

SUSIBA2 GRHNHPKPOPNNRLAGGAVPSNOGGERYDGCASAAADKSSNALSNLANPVHSPGMVEPVPA
Rice GRHNHPKPOPNNRLSAGAVPPIOGGERYDGVATDDKSSNVLSILGNVHTAGMTPEVPG
=====

SUSIBA2 SVSDDDDIDAGGGRPYPGDDATEEDLESKRKRKMSAIDAALMGKPNREPRVVVQTVSEV
Rice SASDDDDNDAGGGRPYPGDDAVEDDLESKRKRKMSAIDAALMGKPNREPRVVVQTVSEV
=====

SUSIBA2 DILDDGYRWRKYGQKVVGKGNPNPRSYKCTSTGCPVRKHVERASHDPKSVITTYEGKHH
Rice DILDDGYRWRKYGQKVVGKGNPNPRSYKCTNTGCPVRKHVERASHDPKSVITTYEGKHH
=====

SUSIBA2 EVPAAARNATHEMSAPPMKNNVVHOLINSNMPSSLGGMRRACEARNYTNQYSQAAEDTISLD
Rice EVPASRNATHEMSAPPMKPVVHPINSNMOGLGGMRRACEPRTFPNQYSQAAESDTISLD
=====

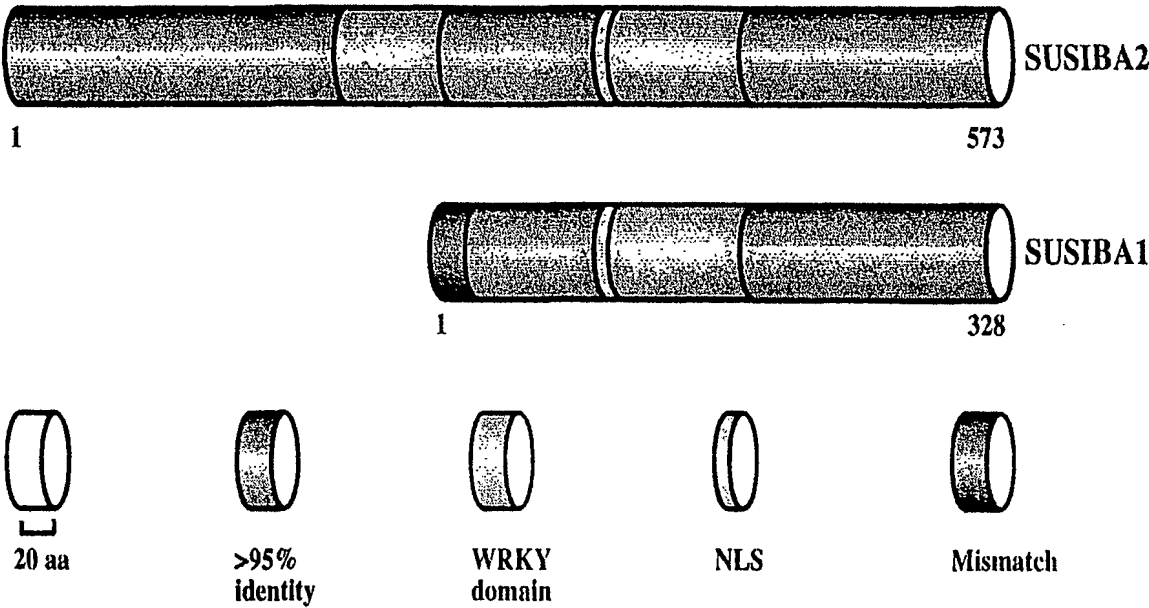
SUSIBA2 LGVGISPNHSDATNQMOSSGPDQMOYQOMTMSNYGNMRHPSSMAAPAVQGNNAARVYGS
Rice LGVGISPNHSDATNQLOSSVSQMOYQOMTMSNYGNMGLP-AMAMPYVAGNAASNLVYGS

SUSIBA2 REEKGNEGFTFRATPMDHSANLCYSAGNLVMGP
Rice REEKPSGFTFRATPMDHSANLCYSAGNLVMGP

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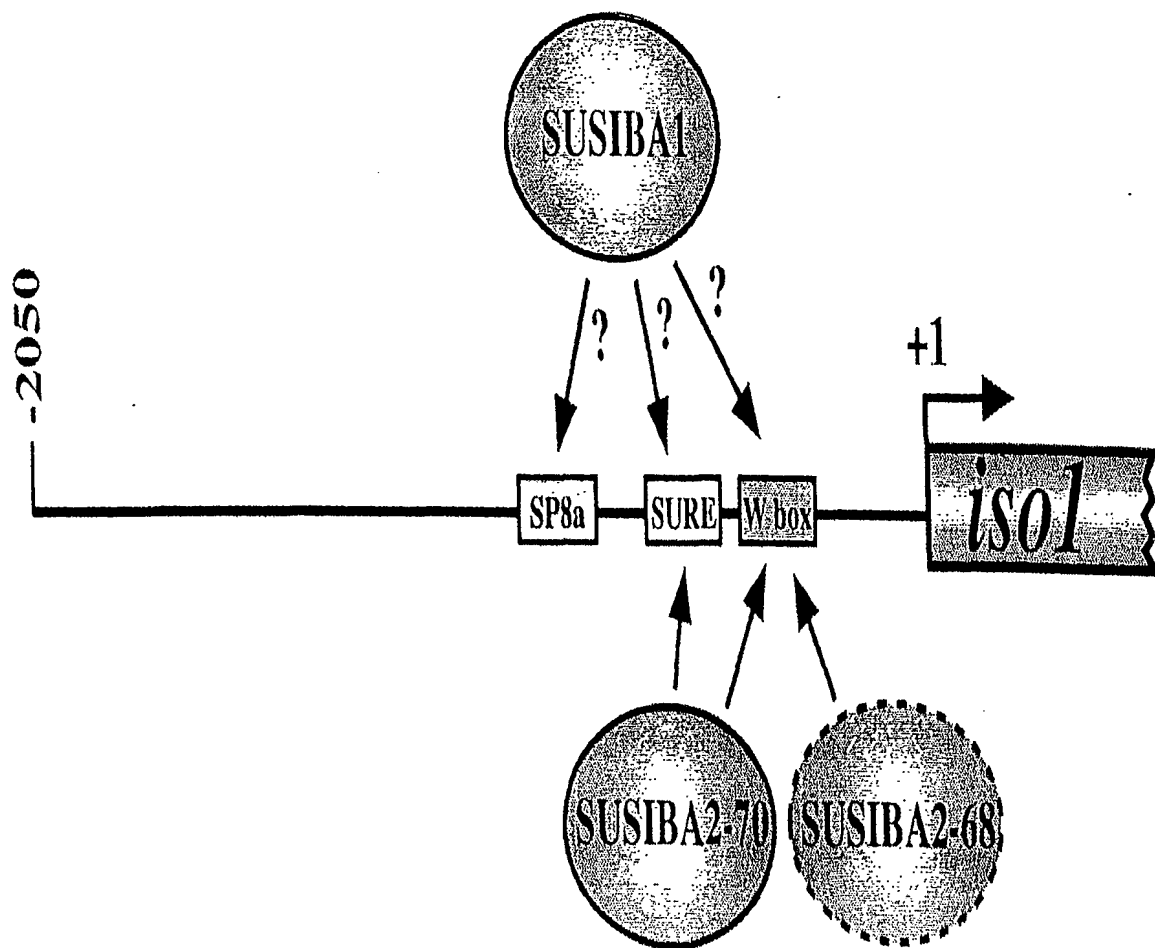
Figure 12



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Figure 13



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Figure 14

SURE-c	-514	-----AAAAAATAAAAGAAATGAAATC-----	-494
SURE-b	-568	-----AATACCAAAAAATAA-TAATAAAA-----	-546
SURE-a	-603	-----CCGAAAAAACTAAGAAAGACCGATG	-578
<i>sbeIIb</i>	-253	-----G-TAATAAAAAA---GG-----G	-240
<i>ssI</i>	-589	-----AAATCCTAAAAAAAATAAT-----	-570
<i>agpaseS</i>	-1132	-----TA-AAATAAAAAC-AAAG-----G	-1116
<i>amy</i>	-1375	-----GCAGAAGATAAAAAAACAA-----	-1356
<i>sbeI</i>	-314	-----ACATA-AAATAAAAAA---AG-----G	-297
<i>sus4</i>	-1287	-----AAATAAAGAGTAGAAAAA-----	-1270
<i>vsp</i>	-759	-----AAAGA-AAATAAAAAATAAAG-----	-778
PI-II	-548	ATGATAATTA-TTTAAAAAACAAGCAAGT-----	-520
ps20	-172	-----AATACTAATAAAGAA-TAGAAAAA-----G	-149

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